

How to Obtain Add Health <u>OMICs</u> Data

02/11/19

addhealth_genetics@unc.edu

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Overview: How to Access Add Health GWAS Data

- The goal of NIH/NICHD-funded grant R03HD097630 (MPIs: Mullan Harris, Avery) is to develop research tools to enable widespread access and use of Add Health genomics (e.g. GWAS, exome etc.) data. This slide set provides tailored instruction in how to access Add Health genomics data.
- <u>Note</u>: Add Health phenotype data are available through: <u>https://www.cpc.unc.edu/projects/addhealth/contracts</u>.
 - See accompanying slide set on accessing additional phenotype data.

dbGaP: NIH Genomics Warehouse

 Add Health GWAS data and accompanying documentation are available from the NIH-sanctioned database of Genotypes and Phenotypes (<u>dbGaP</u>), a repository for archiving, curating, and distributing GWAS data. <u>https://www.ncbi.nlm.nih.gov/gap</u>



Who can Apply for Data Through dbGaP?

- Non-NIH investigators (i.e. Extramural investigators)
 - Extramural Investigators must be permanent employees of their institution at a level equivalent to a tenure-track professor or senior scientist with responsibilities that most likely include laboratory administration and oversight. Laboratory staff and trainees such as graduate students and postdoctoral fellows are not permitted to submit dbGaP project requests.

• NIH Investigators:

- NIH Intramural Investigators must be tenure-track investigators, senior investigators, senior scientists, senior clinicians, or staff scientists.
- NIH extramural scientific staff must have administrative responsibility for the data; have substantial research involvement in the award that generated the data; or need access to carry out research unrelated to their portfolio management responsibilities.

Overview of Process Investigators to Access Datasets in dbGaP



First Step: Obtain an eRA Commons Account

- To log into dbGap and request access to controlled-access datasets, you must have an eRA Commons account (<u>https://era.nih.gov/commons-account-information.cfm</u>).
- If you do not have a pre-existing account, register here: <u>https://era.nih.gov/reg_accounts/register_commons.cfm</u>.



Electronic Research Administration A program of the National Institutes of Health

Identify Add Health GWAS Data and Request Access

• Add Health study accession number: phs001367.v1.p1

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Add Health: Longitudinal Study of a Nationally Representative Sample of Adolescents in Grades 7-12 in the United States during t 1994-95 School Year, Followed into Adulthood with Five Interviews/Surveys in 1995, 1996, 2001-02, 2008, and 2016-18.	he	
dbGaP Study Accession: phs001367.v1.p1 Request Access		
Show BioProject list		
Study Variables Documents Analyses Datasets Molecular Data		
Jump to: Authorized Access Attribution Authorized Requests		

https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs001367.v1.p1

A Completed dbGaP Application:

- Is identified by a Data Access Request (DAR) number and a project number
- Is project-specific. Approval for one project does not carry over to a new project.
- Requires the applicant to review and agree to terms, conditions, and statements of the Add Health Data Use Certification Agreement (October 27, 2015 version, which is currently being updated).

Information Needed for dbGaP Application

- Research statement and nontechnical summary statement describing your planned use of the data specific to your project
- Name of the institutional signing official
- A list of internal investigators at your institution who will share access to the data
- A list of external collaborating investigators
- The name of the information technology (IT) director
- Local Institutional Review Board (IRB) approval.

dbGaP Approved User Code of Conduct

- Investigator(s) will use requested datasets solely in connection with the research project described in the approved Data Access Request for each dataset;
- Investigator(s) will make no attempt to identify or contact individual participants from whom these data were collected without appropriate approvals from the relevant IRBs;
- Investigator(s) will not distribute these data to any entity or individual beyond those specified in the approved Data Access Request;
- Investigator(s) will adhere to computer security practices that ensure that only authorized individuals can gain access to data files;
- Investigator(s) will not submit for publication or any other form of public dissemination analyses
 or other reports on work using or referencing NIH datasets prior to the embargo release date
 listed for the dataset (or dataset version) on dbGaP;
- Investigator(s) acknowledge the Intellectual Property Policies as specified in the Data Use Certification; and,
- Investigator(s) will report any inadvertent data release in accordance with the terms in the Data Use Certification, breach of data security, or other data management incidents contrary to the terms of data access

Begin New Research Project

S NCBI Site map All databases PubMed Search
Logged in as Christy Avery Log out
Beacon Data Browser My Projects My Requests Downloaders My Profile
4y Research Project
Seneral Instructions
 This application will automatically generate a Data Access Request (DAR) number and a project number. Please keep track of this number for future communications with dbGaP and relevant Data Access Committee(s) (DAC) A completed request for data access includes this form as well as a review of and agreement to the terms, conditions, and statements in the Data Use Certification (DUC) for each respective dataset requested. Dataset requests are project-specific. If you were granted access to a dataset(s) for another project, that approval does not carry over to this new proposed project. You must request access to all datasets that you plan to use in the new project. Please note that fields marked as "*" are required fields.
Jefore You Get Started
n order to complete the application for data access you will need to collect the following information:
 A research statement and a nontechnical summary statement describing your planned use of the data. The name of the institutional signing official who will certify the terms of use assurances on behalf of your institution. A list of all internal investigators at your institution who will share access to the data for the proposed research. A list of external collaborating investigators. The name of the information technology (IT) Director. Some datasets may require supplemental documentation to accompany this standard application. Review the DUC* instruction pages for detailed information about how to prepare these materials in a single PDF file.
You can navigate to each study DUC from the public study home page in dbGaP. Look for the "individual-level data" section.
IbGaP APPROVED USER CODE OF CONDUCT
he following is the Code of Conduct that research investigators agree to abide by as Approved Users of data received through the database of Genotypes and Phenotypes (dbGaP). Failure to abide by any term within this Code of Conduct may result in revocation of approved access to any or all datasets being through the database of Genotypes and Phenotypes (dbGaP). Failure to abide by any term within this Code of Conduct may result in revocation of approved access to any or all datasets being through the database of Genotypes and Phenotypes (dbGaP). Failure to abide by any term within this Code of Conduct may result in revocation of approved access to any or all datasets being through the database of Genotypes (dbGaP).
he elements of the NIH Code of Conduct for Data Use include:
 Investigator(s) will use requested datasets solely in connection with the research project described in the approved Data Access Request for each dataset; Investigator(s) will not distribute these data to any entity or individual participants from whom these data were collected without appropriate approvals from the relevant IRBs; Investigator(s) will adhere to computer security practices that ensure that only authorized individuals can gain access to data files; Investigator(s) will not submit for publication or any other form of public dissemination analyses or other reports on work using or referencing NIH datasets prior to the embargo release date listed for the dataset (or dataset version) on dbGaP; Investigator(s) will report any inadvertent data release in accordance with the terms in the Data Use Certification, breach of data security, or other data management incidents contrary to the terms of data access.

<u>NIH</u> Genotype and Phenotype database is a service of NCBI. Please <u>contact us</u> with any questions. National Center for Biotechnology Information | U.S. National Library of Medicine <u>Privacy Notice</u> | <u>Disclaimer</u> | <u>Accessibility</u>

Identify Add Health Study (phs001367.v1.p1)

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For any study that has more than one consent group, there are no overlaps in subject	ts between the consent groups.			
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	phs001374 - VA APOLLO Project - Research for Precision Oncology (RePOP)			
The 100-Person Wellness Project (HPWP) (phs001363.v1.p1)	phs001376 - CD55 Deficiency, Early-Onset Protein-Losing Enteropathy and Thrombosis			
General Research Use (IRB, PUB, COL, NPU) (phs001363.v1.p1.c1), NIGM	phs001377 - Epigenetics of Cocaine and Nicotine Addiction			
	phs001381 - Gut Microbiome and Types of Colorectal Polyps			
	phstu01362 - Reproductive Health in Men and Women with Vasculitis - VCRC 5531			
The Genetic Landscape of Metastasis and Recurrence in HNSCC (phs00100	prisouscent - nine capse to Cancer-Defining the transistion from polypito cancer			
Disease-Specific (Cancer, MDS) (phs001007.v1.p1.c1), NCI DAC	phs001386 - Smoking and the Vaginal Microbiome			
Up for a Challenge: African American Breast Cancer Consortium (AABC) S	phs001389 - Gene Expression and Histone Modification Profiles in GBM Tumors			
Up for a Challenge (Publication required) (phs000851.v1.p1.c1), NCI DAC	phs001391 - OncoArray: Prostate Cancer			
	phs001392 - A Prospective Natural History Study of Diagnosis, Treatment and Outcomes of Children with SCID Disorders - PIDTC 6	901	_	
	nhs001394 - Hypertension-Insulin Resistance Family Study (HTN-IR)		<u> </u>	
Up for a Challenge (Not for Profit Use Only, Publication required)	Use or this data is limited to research described for the National Cancer Institute (NCI) "Up for A Ch	hallenge breast cancer genetic epidemiology competition. The goal of 48	36	

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Accessing New OMICs Files

- Note that the study accession number, phs001367.v1.p1, indexes the version
- New versions are created when new data are uploaded (e.g. exome chip data per R01HD057194). Add Health users with an active dbGaP contract will be alerted to new releases and granted access to newly available data.

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Consent Group	Data Use Limitations	Participants	DAR Status
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Gen ral Research Use (IRB, PUB, GSO) (phs001367.v1,p1.c1), <u>NICHD</u>	Use of the data is limited only by the terms of the model Data Use Certification. Requestor must provide documentation of local IRB approval. Requestor agrees to make results of studies using the data available to the larger scientific community. Use of the data is limited to genetic studies only This consent group requires IRB approval attachment	9974	
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*Descriptive Title of Project		
Please note that coordinated requists by collaborating institutions should each use the same title.		Copy and paste your Research Use Statement and non-technical summary below. All applications must be made in English.
*Research Use Statement (RUS) • A RUS is a brief description of the applicant's proposed use of dbGaP dataset(s). The RUS will be reviewed by all NIH Institutes and Centers responsible for data of	covered by this Data Access Request. Please note that if access is approved, you agree that the RUS	along with your name and institution, will be included on the dbGaP
website widescribe your research project to the public.		
Please make it clear whether you plan to combine requested datasets with other datasets outside of dbGaP, and, if so, whether you plan to analyze these dataset participants. If you are focusing on outcomes or hypotheses that were not the focus of the primary study (or studies), please describe the outcomes you propose	ts independently or together. If you do plan to combine datasets in any way, please describe your pla to examine.	in and also please discuss whether it creates any additional risks to
Investigators do not need to submit a new project request unless the dataset will be used for research outside of the scope of the approved Research Use Staten	nent	
Please enter your RUS in the area below. The RUS should be one or two paragraphs in length and include research objectives, the study design, and an analysis will use them. Examples of RUS can be found at GDS website. Please limit your RUS to 4500 characters.	plan (including the phenotypic characteristics that will be tested for association with genetic variants). If you are requesting multiple datasets, please describe how you
I am requesting permission to use cloud computing to carry out the research as described in my Research Use Statement.		
*Non-technical summary o		
Please enter below a non-technical summary of your RUS suitable for understanding by the general public (written at a high school reading level or below). Pleas	e limit your non-technical summary to 1300 characters.	
*Choose your Signing Official (SD): <		15

Your SO is typically the same person who signs your grant applications and is an individual listed in eRA Commons as a SO for your institution and who has the authority to certify your application on behalf of your institution

Cloud Computing

*Research Use Statement (RUS) 📀

A RUS is a brief description of the applicant's proposed use of dbGaP dataset(s). The RUS will be reviewed by all NIH Institutes and Centers responsible for data covered by this Data Access Request. Please note that if access is approved, you agree that the RUS, along with your name and institution, will be included on the dbGaP website to describe your research project to the public.

Please make it clear whether you plan to combine requested datasets with other datasets outside of dbGaP, and, if so, whether you plan to analyze these datasets independently or together. If you do plan to combine datasets in any way, please describe your plan and also please discuss whether it creates any additional risks to participants. If you are focusing on outcomes or hypotheses that were not the focus of the primary study (or studies), please describe the outcomes you propose to examine.

Investigators do not need to submit a new project request unless the dataset will be used for research outside of the scope of the approved Research Use Statement

Please enter your RUS in the area below. The RUS should be one or two paragraphs in length and include research objectives, the study design, and an analysis plan (including the phenotypic characteristics that will be tested for association with genetic variants). If you are requesting multiple datasets, please describe how you will use them. Examples of RUS can be found at <u>GDS website</u>. Please limit your RUS to 4500 characters.

oxdot I am requesting permission to use cloud computing to carry out the research as described in my Research Use Statement.

- Add Health investigators are currently investigating the feasibility of providing users with virtual machine templates that meet required security protocols when using cloud computing.
- Until these security templates are available, required data security standards for remote compute servers are available here (see section for compute server, not file server):
 - https://www.cpc.unc.edu/research/tools/datasecurity/how-to-secure-a-server
- Outside of the security templates, the Add Health study cannot support costs associated with cloud data storage or analysis.

Do Not Forget Your Decryption Password You Will Need it When You Retrieve the Repository Key!

Create Decryption Password.

The files distributed through the dbGaP system are encrypted. A password is required for decrypting downloaded files. Please provide a decryption password for the project. Valid passwords must be at least 8 ASCII characters long and must contain at least 3 of the following 4 characters:

- upper case letters
- lower case letters
- numbers
- non-alphanumeric characters

*Password for project:	
*Password confirmation	•••••
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IH Genotype and Phenotype data	ase is a service of NCBI. Please contact us with any questions.

Have Your IT Director and Collaborators Identified, Including Contact Information

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An information technology (IT) director's (or designee's) contact infor	rmation is required to ensure data security	policies and procedures are in place. This in	dividual must have the authority to vouch for the IT ca	apabilities at your institution.	
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NIH Genotype and Phenotype database is a service of NCBI. Please <u>contact us</u> with any National <u>Center for Biotechnology Information</u> <u>U.S. National Library of Medicine</u> <u>Privacy Notice</u> <u>Dicclaimer</u> <u>Accessibility</u>	/ questions.				

Add Heath Requires IRB Approval Prior to dbGaP Submission

Consent Group	Data Use Limitations		Participants
Add Health: The National Longitudinal Study of Adolescent to Adult Health (Add Health) (p	hs001367.v1.p1)		
✓ General Research Use (IRB, PUB, GSO) (phs001367.v1.p1.c1), NICHD	Use of the data is limited only by the terms of the model Data Use Certification. Requestor must provide decrementation of head TDB serviced. The service heads we result of studies using the data available to the larger scientific community. Use of the data is limited to genetic studies only. This consent group requires IRB approval attachment	9974	
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• Either expedited or exempt IRB approval is acceptable.

Publication of Genomic Summary Results



- Given the sensitivity of Add Health, genomic summary results (GSR) that contain Add Health data should be provided only through controlled-access data access request and review procedures (e.g. through dbGaP).
- For more information, see:

https://grants.nih.gov/grants/guide/notice-files/NOT-OD-19-023.html

Submit Application!

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after you have sub	nitted your application for review you will have to contact your <u>SO</u> with a request to return it for your revision.		To approve: Check the boxes below to attach your electronic signature acknowledging agreement to the terms.			
After approval by	pur <u>SO</u> , each application will be sent to the appropriate Data Access Committee (DAC). Multiple <u>DAC</u> s may need to evaluate your application.					
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To Download dbGaP data; Download NIH SRA Toolkit

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• 🛃 MacOS 64	bit architecture		 <u>BioProject & BioSample</u>
• 🛃 MacOS 32	bit architecture		 <u>SRA Metadata Overview</u>
• 🛃 MS Windo	vs 64 bit architecture		 <u>SRA File Upload</u>
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SRA Submission Porta

Navigate to https://www.ncbi.nlm.nih.gov/sra/docs/toolkitsoft/ Download relevant architecture (CentOS or Ubuntu Linux) tar -xvzf /path/to/file/sratoolkit.current-ubuntu64.tar.gz

Select files on dbGaP

- Navigate to dbGaP <u>https://dbgap.ncbi.nlm.nih.gov/aa/wga.cgi?page=login</u> and login using the eRA account credentials
- Click on "My Requests" tab. The list of Approved Requests is under "Approved" sub-tab. (slide 24)
- Find the table row of approved dataset (phs001367.v1.p1), click on the link named "Request Files" in the "Actions" column.
- On the "Access Request" page, go to the "Phenotype and Genotype files" sub-tab and click on the "dbGaP File Selector" link.
- Add/remove files using the facets listed in the left panel facet manager. From the right panel file list, select/unselect files by checking/unchecking checkboxes in front of the file names. (slide 25)
- Once the files are selected (checked), click on the "Cart File" button (on the upper part of the page) and save the cart file (.kart).

dbGaP Approved Requests

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کړ db GaP			Logged in as Kathleen Harris Log out
genotypes and phenotypes Browse/Search	Authorized Access Help		
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Request List			
#	Study, Consent	Status Expiration	Actions
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dbGaP File Selector

S NUBL ODGAP FIle Selector	• Help Sermalink	ζ			
 Facets Content type File name Size Data category 	 Hide common fiel Consent: Downloaded: Release date: Study accession: 	 Hide common fields Consent: GRU-IRB-PUB-GSO Downloaded: no Release date: 2018-09-12 Study accession: phs001367.v1.p1 			
File accession		Files	Size	🗎 Download	
Genotype platform	Total:	25	637.95 Gb	Files Table	
	Selected:			Cart File	

25 Files found

0/0	Content type	File name	Size	Description	Data category	Embargo date	File accession	Genotype platform
	Use contents	Study_Report.phs001367.AddHealth.v1.p1.MULTI.pdf	55.2 kb	Master stud consent category).	StudyMeta	No Embargo	phs001367.v1.p1	N/A
	Use contents	Release_Notes.phs001367.AddHealth.v1.p1.MULTI.pdf	144.1 kb	Release nownload component set	StudyMeta	No Embargo	phs001367.v1.p1	N/A
	Use contents	manifest_pGRU-IRB-PUB-GSO.pdf	41.8 kb	Release nownload component set	StudyMeta	No Embargo	phs001367.v1.p1	N/A
	Phenotype data-dictionary	phs001367ubject.data_dict.xml	734b	pht008245ataset pht008245.v1.	Phenotype	2018-09-12	phs001367.v1.p1	N/A
	Phenotype individual-auxiliary	phs001367Subject.MULTI.txt.gz	67.2 kb	pht008245onsent - Information	Phenotype	2018-09-12	pht008245.v1.p1	N/A
	Phenotype variable-report	phs001367bject.var_report.xml	2.0 kb	pht008245ataset pht008245.v1.	Phenotype	2018-09-12	pht008245.v1.p1	N/A
	Phenotype data-dictionary	phs001367digree.data_dict.xml	1.1 kb	pht008246ataset pht008246.v1.	Phenotype	2018-09-12	phs001367.v1.p1	N/A
	Phenotype individual-pedigree	phs001367edigree.MULTI.txt.gz	29.5 kb	pht008246.v1: Pedigree Information	Phenotype	2018-09-12	pht008246.v1.p1	N/A
	Phenotype variable-report	phs001367igree.var_report.xml	4.3 kb	pht008246ataset pht008246.v1.	Phenotype	2018-09-12	pht008246.v1.p1	N/A
	Phenotype data-dictionary	phs001367Sample.data_dict.xml	569b	pht008247ataset pht008247.v1.	Phenotype	2018-09-12	phs001367.v1.p1	N/A
	Phenotype individual-auxiliary	phs001367Sample.MULTI.txt.gz	284.1 kb	pht008247mple Use information	Phenotype	2018-09-12	pht008247.v1.p1	N/A
	Phenotype variable-report	phs001367ample.var_report.xml	2.2 kb	pht008247ataset pht008247.v1.	Phenotype	2018-09-12	pht008247.v1.p1	N/A
	Phenotype data-dictionary	phs001367otypes.data_dict.xml	1.4 kb	pht008248ataset pht008248.v1.	Phenotype	2018-09-12	phs001367.v1.p1	N/A
	Phenotype variable-report	phs001367types.var_report.xml	9.4 kb	pht008248ataset pht008248.v1.	Phenotype	2018-09-12	pht008248.v1.p1	N/A
	Phenotype individual-traits	phs001367U-IRB-PUB-GSO.txt.gz	170.9 kb	pht008248 height information.	Phenotype	2018-09-12	pht008248.v1.p1	N/A
	Phenotype data-dictionary	phs001367ibutes.data_dict.xml	930b	pht008249ataset pht008249.v1.	Phenotype	2018-09-12	phs001367.v1.p1	N/A
	Phenotype variable-report	phs001367butes.var_report.xml	3.7 kb	pht008249ataset pht008249.v1.	Phenotype	2018-09-12	pht008249.v1.p1	N/A
	Phenotype individual-traits	phs001367U-IRB-PUB-GSO.txt.gz	70.3 kb	pht008249 source of samples.	Phenotype	2018-09-12	pht008249.v1.p1	N/A
	Genotype sample-information	phg001069.v1.AddHealth.sample-info.MULTI.tar.gz	247.2 kb	Informatiofiles in the release	Genotype	2018-09-12	phg001069.v1	NULL
	Genotype calls-matrix-format	phg001069U-IRB-PUB-GSO.tar.gz	846.3 Mb	Set of texa particular consent	Genotype	2018-09-12	phg001069.v1	NULL
	Genotype qc	phg001069v1-0_H.MULTI.tar.gz	6.4 Mb	Marker andrequnecy, and others	Genotype	2018-09-12	phg001069.v1	NULL
	Genotype imputed-data	phg001099PUB-GSO.set1.tar.gz	518.5 Gb	Imputed geme and subject group	Genotype	2018-09-12	phg001099.v1	NULL
	Genotype imputed-data	phg001099PUB-GSO.set2.tar.gz	118.7 Gb	Imputed geme and subject group	Genotype	2018-09-12	phg001099.v1	NULL
	Genotype sample-information	phg001099.v1.AddHealth.sample-info.MULTI.tar.gz	2.4 Mb	Informatiofiles in the release	Genotype	2018-09-12	phg001099.v1	NULL

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Create directory for results

- Naming convention isn't optional, requires lower case 'ncbi'
- Create a directory titled 'ncbi' at root
- cd ~; mkdir ncbi; cd ncbi
- Move .kart file into ncbi directory ie. *mv cart_prj19687_201902081009 ./*

prefetch dbGaP files

- Use the 'prefetch' utility to download the data files specified by the cart file.
- /path-to-sratoolkit-install-dir/bin/prefetch -t ascp -a cart_prj19687_201902081009
- Depending on the size, you might need to specify '-max-size 100000000'
- This will generate a directory at ~/ncbi/dbGaP-19687 which contains files, sra, wgs, nannot, and refseq
- All data and metadata will be in ~/ncbi/dbGaP-19687/files
- All files will be encrypted and end *.ncbi_enc

Decrypt files with vdb-config

- Use vdb-config tool to decrypt them
- ncbi/dbGaP_19687/files\$ /path/to/sratoolkit.2.9.4-centos_linux64/bin/vdbconfig —i
- This will open an interactive vdb-config session. (slide 29)
- Import your repository key (NGC file), box 4 (slide 30)
- Select your folder eg. ncbi/dbGaP-19687, tab down to 'change' (slide 31)
- Click save, box 6
- Click exit, box 7

vdb-config interface

vdb-config				
<pre>[X] Enable Remote Access (1) [X] Enable Local File Caching (2) [] Use Proxy [Change]</pre>	<pre>[Save (6)] [Exit (7)] [Reload (8)] [Standard Settings (9)]</pre>			
[Import Repository Key (4)] [Workspace Name	Set Default Import Path (5)]			
Public [Change] /home/joeuser/ncbi/public			
Press the number in (X) as a shorto	cut			
Press SPACE ENTER to enable/disable access to the servers at NCBI				

Assign repository key

[X]	Enable Remote Access (1)	[Save (6)] [Exit (7)]		
[X	select file			
	/ifs/sec/cpc/addhealth/users/belevitt/exome			
]	directories: [] files sratoolkit.2.9.4-centos_linux64			
[Wo				
db				
	files: prj_19687.ngc			
	[OK] [Cancel (ESC-ESC)]			
Pre	Press the number in (X) as a shortcut			

Press SPACE | ENTER to import a dbGaP project

Decrypt files

\	/db-config				
[X]] Enable Remote Access (1)	[Save (6)] [Exit (7)]			
[X	select directory				
	/ifs/sec/cpc/addhealth/users/belevitt/ncbi/dbGaP-19687/files				
1	directories:				
1	oc				
	imputed				
	phg001099.v1.AddHealth.marker-info.MULTI				
1	phg001099.v1.AddHealth.sample-info.MULTI sample				
Wo	tarballs				
db					
	[OK] [Cancel (ESC-ESC)] [Goto] [Create Dir]				
Pre	Press the number in (X) as a shortcut				

Press SPACE | ENTER to change location for this dbGaP repository

Additional resources for downloading dbGaP data

https://www.ncbi.nlm.nih.gov/books/NBK36439/ GaP FAQ Archive: Downloading Data https://dbgap.ncbi.nlm.nih.gov/aa/wga.cgi?page=login dbGaP authorized access point https://www.biostars.org/p/316506/ option for prefetch large files https://github.com/ncbi/sra-tools/wiki/Toolkit-Configuration how to navigate the vdb-config utility

Additional Add Health OMICs Resources

- Sign up for the addhealthomics listserv. To subscribe/join:
 - 1. Send an email to <u>subscribe-addhealthomics@listserv.unc.edu</u> with no message body
 - 2. Wait for addhealthomics confirmation email
 - 3. Click the confirm link the email
- <u>Future resources</u> that will aid users in accessing, understanding, analyzing, and interpreting Add Health genomics data, prioritizing GWAS data, will be posted at:
 - <u>https://www.biostars.org/t/addhealthomics/</u>
 - <u>https://www.cpc.unc.edu/projects/addhealth/documentation/omics</u>